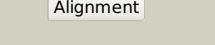
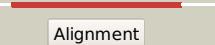
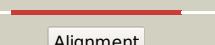
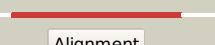


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD3168 (-) _3536099_3537235
Date	Thu Aug 8 16:20:35 BST 2019
Unique Job ID	fbf1de0e1eb43f73

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3attA_</a>			100.0	100	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of rv3168 with atp
2	<a href="#">c3dxdpA_</a>			100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative aminoglycoside phosphotransferase2 (reut_a1007) from ralstonia eutropha jmp134 at 2.32 a resolution
3	<a href="#">c3ovcA_</a>			100.0	17	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A; <b>PDB Molecule:</b> hygromycin-b 4-o-kinase; <b>PDBTitle:</b> crystal structure of aminoglycoside phosphotransferase aph(4)-ia
4	<a href="#">c5uxbA_</a>			100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> macrolide 2'-phosphotransferase mph; <b>PDBTitle:</b> crystal structure of macrolide 2'-phosphotransferase mph from2 brachybacterium faecium, apoenzyme
5	<a href="#">c6ef6A_</a>			100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> aminoglycoside phosphotransferase; <b>PDBTitle:</b> structure of the microcompartment-associated aminopropanol kinase
6	<a href="#">c3csvA_</a>			100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> aminoglycoside phosphotransferase; <b>PDBTitle:</b> crystal structure of a putative aminoglycoside phosphotransferase2 (yp_614837.1) from silicibacter sp. tm1040 at 2.15 a resolution
7	<a href="#">c5igrA_</a>			100.0	18	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A; <b>PDB Molecule:</b> macrolide 2'-phosphotransferase; <b>PDBTitle:</b> macrolide 2'-phosphotransferase type i - complex with gdp and 2 oleandomycin
8	<a href="#">c3lzhA_</a>			100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> aph(2")-id/aph(2")-iva; <b>PDBTitle:</b> crystal structure of aminoglycoside phosphotransferase aph(2")-2 id/aph(2")-iva
9	<a href="#">c4h05B_</a>			100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> aminoglycoside-o-phosphotransferase viii; <b>PDBTitle:</b> crystal structure of aminoglycoside-3'-phosphotransferase of type viii
10	<a href="#">c3tdvB_</a>			100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> gentamicin resistance protein; <b>PDBTitle:</b> structure of the gdp complex of wild-type aminoglycoside 2'-2 phosphotransferase-iiia
11	<a href="#">c3jr1A_</a>			100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative fructosamine-3-kinase; <b>PDBTitle:</b> crystal structure of putative fructosamine-3-kinase (yp_719053.1) from2 haemophilus somnus 129pt at 2.32 a resolution

12	<a href="#">c6fucA</a>		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> aminoglycoside phosphotransferase; <b>PDBTitle:</b> structure of aminoglycoside phosphotransferase aph(3')-id from2 streptomyces rimosus atcc10970	
13	<a href="#">c3r78B</a>		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> aminoglycoside 3'-phosphotransferase aph(1-iab); <b>PDBTitle:</b> crystal structure of the aminoglycoside phosphotransferase aph(3')-ia,2 atp-bound	
14	<a href="#">d1j7la</a>		100.0	16	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases	
15	<a href="#">c5sigwA</a>		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> macrolide 2'-phosphotransferase ii; <b>PDBTitle:</b> macrolide 2'-phosphotransferase type ii - complex with gdp and2 clarithromycin	
16	<a href="#">c3f7wA</a>		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative fructosamine-3-kinase; <b>PDBTitle:</b> crystal structure of putative fructosamine-3-kinase (yp_290396.1) from2 thermobifida fusca yx-er1 at 1.85 a resolution	
17	<a href="#">d1nd4a</a>		100.0	16	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases	
18	<a href="#">d2pula1</a>		100.0	16	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases	
19	<a href="#">c2pywA</a>		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of a. thaliana 5-methylthioribose kinase in complex with adp2 and mtr	
20	<a href="#">d2ppqa1</a>		100.0	13	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases	
21	<a href="#">d1zyla1</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> APH phosphotransferases
22	<a href="#">c4r77A</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> choline kinase; <b>PDBTitle:</b> crystal structure of choline kinase lica from streptococcus pneumoniae
23	<a href="#">c3mesB</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> choline kinase; <b>PDBTitle:</b> crystal structure of choline kinase from cryptosporidium2 parvum iowa ii, cgd3_2030
24	<a href="#">c3c5iD</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> choline kinase; <b>PDBTitle:</b> crystal structure of plasmodium knowlesi choline kinase, pkh_134520
25	<a href="#">c4orkB</a>	Alignment	not modelled	100.0	9	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> bifunctional aac/aph; <b>PDBTitle:</b> crystal structure of the phosphotransferase domain of the bifunctional2 aminoglycoside resistance enzyme aac(6')-ie-aph(2')-ia
26	<a href="#">c3hamA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> aminoglycoside phosphotransferase; <b>PDBTitle:</b> structure of the gentamicin-aph(2")-iia complex
27	<a href="#">c1nw1A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> choline kinase (49.2 kd); <b>PDBTitle:</b> crystal structure of choline kinase
28	<a href="#">d1nw1a</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Choline kinase
<b>PDB header:</b> transferase						

29	<a href="#">c4ockA</a>	Alignment	not modelled	99.9	11	<b>Chain: A: PDB Molecule:</b> n-acetylhexosamine 1-phosphate kinase; <b>PDBTitle:</b> n-acetylhexosamine 1-phosphate kinase in complex with glcnac and2 amppnp
30	<a href="#">c2ig7A</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> choline/ethanolamine kinase; <b>PDBTitle:</b> crystal structure of human choline kinase b
31	<a href="#">c3dxqB</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain: B: PDB Molecule:</b> choline/ethanolamine kinase family protein; <b>PDBTitle:</b> crystal structure of choline/ethanolamine kinase family protein2 (np_106042.1) from mesorhizobium loti at 2.55 a resolution
32	<a href="#">c3f2rA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> choline kinase alpha; <b>PDBTitle:</b> crystal structure of human choline kinase alpha in complex with2 hemicholinium-3
33	<a href="#">c3i0oA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> spectinomycin phosphotransferase; <b>PDBTitle:</b> crystal structure of spectinomycin phosphotransferase,2 aph(9)-ia, in complex with adp and spectinomycin
34	<a href="#">c2ckpA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> choline kinase alpha; <b>PDBTitle:</b> crystal structure of human choline kinase alpha-2 in2 complex with adp
35	<a href="#">c2ckpB</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transferase <b>Chain: B: PDB Molecule:</b> choline kinase alpha; <b>PDBTitle:</b> crystal structure of human choline kinase alpha-2 in2 complex with adp
36	<a href="#">c2q83A</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> ytaa protein; <b>PDBTitle:</b> crystal structure of ytaa (2635576) from bacillus subtilis at 2.50 a2 resolution
37	<a href="#">c3f2rB</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transferase <b>Chain: B: PDB Molecule:</b> choline kinase alpha; <b>PDBTitle:</b> crystal structure of human choline kinase alpha in complex with2 hemicholinium-3
38	<a href="#">c2qg7A</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> ethanolamine kinase pv091845; <b>PDBTitle:</b> plasmodium vivax ethanolamine kinase pv091845
39	<a href="#">c4pdyA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> aminoglycoside phosphotransferase; <b>PDBTitle:</b> crystal structure of aminoglycoside phosphotransferase from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
40	<a href="#">c5jy7K</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> isomerase/transferase <b>Chain: K: PDB Molecule:</b> maltokinase; <b>PDBTitle:</b> complex of mycobacterium smegmatis trehalose synthase with maltokinase
41	<a href="#">c4o7oB</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase <b>Chain: B: PDB Molecule:</b> maltokinase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis maltose kinase mak
42	<a href="#">c5jy7I</a>	Alignment	not modelled	99.6	12	<b>PDB header:</b> isomerase/transferase <b>Chain: I: PDB Molecule:</b> maltokinase; <b>PDBTitle:</b> complex of mycobacterium smegmatis trehalose synthase with maltokinase
43	<a href="#">c4wzyA</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> maltokinase; <b>PDBTitle:</b> structure of mycobacterial maltokinase, the missing link in the2 essential glge-pathway (atp complex)
44	<a href="#">c3en9B</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> hydrolase <b>Chain: B: PDB Molecule:</b> o-sialoglycoprotein endopeptidase/protein kinase; <b>PDBTitle:</b> structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
45	<a href="#">c2pzIA</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> probable serine/threonine-protein kinase pkng; <b>PDBTitle:</b> crystal structure of protein kinase pkng from mycobacterium2 tuberculosis in complex with tetrahydrobenzothiophene ax20017
46	<a href="#">c4pedA</a>	Alignment	not modelled	99.2	10	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> chaperone activity of bc1 complex-like, mitochondrial; <b>PDBTitle:</b> mitochondrial adck3 employs an atypical protein kinase-like fold to2 enable coenzyme q biosynthes
47	<a href="#">c6hwIB</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> transferase <b>Chain: B: PDB Molecule:</b> glucosamine kinase; <b>PDBTitle:</b> glucosamine kinase in complex with glucosamine, adp and inorganic2 phosphate
48	<a href="#">c5yk2A</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> transport protein <b>Chain: A: PDB Molecule:</b> probable conserved atp-binding protein abc transporter; <b>PDBTitle:</b> the complex structure of rv3197-erythromycin from mycobacterium2 tuberculosis
49	<a href="#">c6g51v</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> ribosome <b>Chain: V: PDB Molecule:</b> 40s ribosomal protein s21; <b>PDBTitle:</b> cryo-em structure of a late human pre-40s ribosomal subunit - state d
50	<a href="#">c6fdnA</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> nuclear protein <b>Chain: A: PDB Molecule:</b> serine/threonine-protein kinase rio2; <b>PDBTitle:</b> rio2 structure
51	<a href="#">c6g4jA</a>	Alignment	not modelled	98.8	18	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> probable serine/threonine-protein kinase yabt; <b>PDBTitle:</b> structure of the protein kinase yabt from bacillus subtilis in complex2 with an alpharep crystallization helper
52	<a href="#">c4uw0A</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> wbdd; <b>PDBTitle:</b> low resolution structure of wbdd with c-terminal bundle ordered to2 residue 505
53	<a href="#">c6g51A</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> lipopolysaccharide core heptose(i) kinase

53	<a href="#">c0una_</a>	Alignment	not modelled	98.7	17	rfap; <b>PDBTitle:</b> waap in complex with acyl carrier protein
54	<a href="#">c4azwA_</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> wbdd; <b>PDBTitle:</b> crystal structure of monomeric wbdd.
55	<a href="#">c5ebzF_</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> F: <b>PDB Molecule:</b> inhibitor of nuclear factor kappa-b kinase subunit alpha; <b>PDBTitle:</b> crystal structure of human ikk1
56	<a href="#">c4azsA_</a>	Alignment	not modelled	98.7	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase wbdd; <b>PDBTitle:</b> high resolution (2.2 a) crystal structure of wbdd.
57	<a href="#">c4c0tA_</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> likely protein kinase; <b>PDBTitle:</b> candida albicans pkh kinase domain
58	<a href="#">c4ww7A_</a>	Alignment	not modelled	98.6	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ekc/keops complex subunit bud32; <b>PDBTitle:</b> crystal structure of binary complex bud32-cgi121 in complex with amp
59	<a href="#">c3qa8H_</a>	Alignment	not modelled	98.6	18	<b>PDB header:</b> immune system, signalling protein <b>Chain:</b> H: <b>PDB Molecule:</b> mgc80376 protein; <b>PDBTitle:</b> crystal structure of inhibitor of kappa b kinase beta
60	<a href="#">c3pfqA_</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c beta type; <b>PDBTitle:</b> crystal structure and allosteric activation of protein kinase c beta2 ii
61	<a href="#">c2vwiC_</a>	Alignment	not modelled	98.5	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> serine/threonine-protein kinase osr1; <b>PDBTitle:</b> structure of the osr1 kinase, a hypertension drug target
62	<a href="#">c4im2A_</a>	Alignment	not modelled	98.5	15	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase tbk1; <b>PDBTitle:</b> structure of tank-binding kinase 1
63	<a href="#">c3qa8A_</a>	Alignment	not modelled	98.5	19	<b>PDB header:</b> immune system, signalling protein <b>Chain:</b> A: <b>PDB Molecule:</b> mgc80376 protein; <b>PDBTitle:</b> crystal structure of inhibitor of kappa b kinase beta
64	<a href="#">c6ccfB_</a>	Alignment	not modelled	98.5	13	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> calcium/calmodulin-dependent protein kinase kinase 1; <b>PDBTitle:</b> crystal structure of the human camkk1a in complex with hesperadin
65	<a href="#">c4czuC_</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> cbl-interacting serine/threonine-protein kinase 23; <b>PDBTitle:</b> crystal structure of the kinase domain of cipk23 t190d mutant
66	<a href="#">c2fo0A_</a>	Alignment	not modelled	98.5	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase abl1 (1b isoform); <b>PDBTitle:</b> organization of the sh3-sh2 unit in active and inactive forms of the 2c-abl tyrosine kinase
67	<a href="#">c4gygA_</a>	Alignment	not modelled	98.4	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rio2 kinase; <b>PDBTitle:</b> crystal structure of the rio2 kinase from chaetomium thermophilum
68	<a href="#">c1tqmA_</a>	Alignment	not modelled	98.4	20	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of a. fulgidus rio2 serine protein kinase bound to2 amppnp
69	<a href="#">d1zara2</a>	Alignment	not modelled	98.4	20	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> RIO1-like kinases
70	<a href="#">c2j0kB_</a>	Alignment	not modelled	98.4	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> focal adhesion kinase 1; <b>PDBTitle:</b> crystal structure of a fragment of focal adhesion kinase containing2 the ferm and kinase domains.
71	<a href="#">c4yhjA_</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> g protein-coupled receptor kinase 4; <b>PDBTitle:</b> structure and function of the hypertension variant a486v of g protein-2 coupled receptor kinase 4 (grk4)
72	<a href="#">c3q60A_</a>	Alignment	not modelled	98.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rop5b; <b>PDBTitle:</b> crystal structure of virulent allele rop5b pseudokinase domain bound2 to atp
73	<a href="#">c4ci6B_</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> transferase/structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein kinase yopo; <b>PDBTitle:</b> mechanisms of crippling actin-dependent phagocytosis by yopo
74	<a href="#">c5uuuA_</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> beta-adrenergic receptor kinase 1; <b>PDBTitle:</b> design, synthesis, and evaluation of the first selective and potent g-2 protein-coupled receptor kinase 2 (grk2) inhibitor for the potential3 treatment of heart failure
75	<a href="#">c5dfzB_</a>	Alignment	not modelled	98.3	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase vps15; <b>PDBTitle:</b> structure of vps34 complex ii from s. cerevisiae.
76	<a href="#">c4eutA_</a>	Alignment	not modelled	98.3	15	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase tbk1; <b>PDBTitle:</b> structure of bx-795 complexed with unphosphorylated human tbk1 kinase-2 uld domain
77	<a href="#">c1oplA_</a>	Alignment	not modelled	98.3	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase; <b>PDBTitle:</b> structural basis for the auto-inhibition of c-abl tyrosine2 kinase
78	<a href="#">c3ckxA_</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase 24; <b>PDBTitle:</b> crystal structure of sterile 20-like kinase 3 (mst3, stk24) in complex2 with staurosporine

79	<a href="#">c4otpA</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase rio1; <b>PDBTitle:</b> crystal structure of the catalytic domain of the human rik1 atypical protein kinase in complex with adp/mg2+
80	<a href="#">c3nyoB</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> g protein-coupled receptor kinase 6; <b>PDBTitle:</b> crystal structure of g protein-coupled receptor kinase 6 in complex2 with amp
81	<a href="#">c4cfhA</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5'-amp-activated protein kinase catalytic subunit alpha-1; <b>PDBTitle:</b> structure of an active form of mammalian ampk
82	<a href="#">c4wb7B</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> dnaj homolog subfamily b member 1,camp-dependent protein <b>PDBTitle:</b> crystal structure of a chimeric fusion of human dnaj (hsp40) and camp-2 dependent protein kinase a (catalytic alpha subunit)
83	<a href="#">c4i6hA</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase plk2; <b>PDBTitle:</b> selective & brain-permeable polo-like kinase-2 (plk-2) inhibitors that2 reduce alpha-synuclein phosphorylation in rat brain
84	<a href="#">c4eqmE</a>	Alignment	not modelled	98.2	14	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> protein kinase; <b>PDBTitle:</b> structural analysis of staphylococcus aureus serine/threonine kinase2 pknb
85	<a href="#">c1ym7C</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-adrenergic receptor kinase 1; <b>PDBTitle:</b> g protein-coupled receptor kinase 2 (grk2)
86	<a href="#">c4o96D</a>	Alignment	not modelled	98.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> type iii effector protein kinase; <b>PDBTitle:</b> 2.60 angstrom resolution crystal structure of a protein kinase domain2 of type iii effector nleh2 (ecs1814) from escherichia coli o157:h73 str. sakai
87	<a href="#">c3tkuB</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase mrck beta; <b>PDBTitle:</b> mrck beta in complex with fasudil
88	<a href="#">c3otvC</a>	Alignment	not modelled	98.2	11	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> probable conserved transmembrane protein; <b>PDBTitle:</b> crystal structure of the intracellular domain of rv3910 from2 mycobacterium tuberculosis
89	<a href="#">c4y93A</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> non-specific protein-tyrosine kinase,non-specific protein- <b>PDBTitle:</b> crystal structure of the ph-th-kinase construct of bruton's tyrosine2 kinase (ltk)
90	<a href="#">c4wnkA</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> g protein-coupled receptor kinase 5; <b>PDBTitle:</b> crystal structure of bovine g protein coupled-receptor kinase 5 in2 complex with ccg215022
91	<a href="#">c4dn5A</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mitogen-activated protein kinase kinase 14; <b>PDBTitle:</b> crystal structure of nf-kb-inducing kinase (nik)
92	<a href="#">c4myiA</a>	Alignment	not modelled	98.2	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cgmp-dependent protein kinase, putative; <b>PDBTitle:</b> crystal structure of ppx_084705
93	<a href="#">c1zp9A</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rio1 kinase; <b>PDBTitle:</b> crystal structure of full-length a.fulgidus rio1 serine kinase bound2 to atp and mn2+ ions.
94	<a href="#">c3c4wB</a>	Alignment	not modelled	98.1	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> rhodopsin kinase; <b>PDBTitle:</b> crystal structure of g protein coupled receptor kinase 1 bound to atp2 and magnesium chloride at 2.7a
95	<a href="#">c2acxB</a>	Alignment	not modelled	98.1	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> g protein-coupled receptor kinase 6; <b>PDBTitle:</b> crystal structure of g protein coupled receptor kinase 6 bound to2 amppnp
96	<a href="#">c3c4yA</a>	Alignment	not modelled	98.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhodopsin kinase; <b>PDBTitle:</b> crystal structure of apo form of g protein coupled receptor kinase 12 at 7.51a
97	<a href="#">c2ozoA</a>	Alignment	not modelled	98.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase zap-70; <b>PDBTitle:</b> autoinhibited intact human zap-70
98	<a href="#">c4cdsA</a>	Alignment	not modelled	98.1	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine kinase as - a common ancestor of src and abl; <b>PDBTitle:</b> tyrosine kinase as - a common ancestor of src and abl
99	<a href="#">c5ckwA</a>	Alignment	not modelled	98.1	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> legk4; <b>PDBTitle:</b> crystal structure of legk4_amppnp kinase
100	<a href="#">c1k9aB</a>	Alignment	not modelled	98.1	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> carboxyl-terminal src kinase; <b>PDBTitle:</b> crystal structure analysis of full-length carboxyl-terminal2 src kinase at 2.5 a resolution
101	<a href="#">c1mrub</a>	Alignment	not modelled	98.1	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable serine/threonine-protein kinase pknb; <b>PDBTitle:</b> intracellular ser/thr protein kinase domain of mycobacterium2 tuberculosis pknb.
102	<a href="#">c5d7vD</a>	Alignment	not modelled	98.1	11	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> protein-tyrosine kinase 6; <b>PDBTitle:</b> crystal structure of ptk6 kinase domain
103	<a href="#">c5ncIA</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase cbk1; <b>PDBTitle:</b> crystal structure of the cbk1-mob2 kinase-coactivator

						complex with an2 ssd1 peptide
104	<a href="#">c4xi2A</a>	Alignment	not modelled	98.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase btk; <b>PDBTitle:</b> crystal structure of an auto-inhibited form of bruton's tyrosine2 kinase
105	<a href="#">c6jkmA</a>	Alignment	not modelled	98.0	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mitotic checkpoint control protein kinase bub1; <b>PDBTitle:</b> crystal structure of babr1 kinase domain
106	<a href="#">c2h8hA</a>	Alignment	not modelled	98.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase src; <b>PDBTitle:</b> src kinase in complex with a quinazoline inhibitor
107	<a href="#">c6m7zE</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> bradyzoite pseudokinase 1; <b>PDBTitle:</b> a divergent kinase lacking the glycine-rich loop regulates membrane2 ultrastructure of the toxoplasma parasitophorous vacuole
108	<a href="#">c4btfa</a>	Alignment	not modelled	98.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mixed lineage kinase domain-like protein; <b>PDBTitle:</b> structure of mlkl
109	<a href="#">c6emlr</a>	Alignment	not modelled	98.0	15	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 40s ribosomal protein s2; <b>PDBTitle:</b> cryo-em structure of a late pre-40s ribosomal subunit from2 saccharomyces cerevisiae
110	<a href="#">c4bwpa</a>	Alignment	not modelled	98.0	14	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> pab-dependent poly(a)-specific ribonuclease subunit pan-3; <b>PDBTitle:</b> structure of drosophila melanogaster pan3 pseudokinase
111	<a href="#">c4mvfA</a>	Alignment	not modelled	97.9	14	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-dependent protein kinase 2; <b>PDBTitle:</b> crystal structure of plasmodium falciparum cdk2 complexed with2 inhibitor staurosporine
112	<a href="#">c2c30A</a>	Alignment	not modelled	97.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase pak 6; <b>PDBTitle:</b> crystal structure of the human p21-activated kinase 6
113	<a href="#">c4y83B</a>	Alignment	not modelled	97.9	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mitogen-activated protein kinase kinase 8; <b>PDBTitle:</b> crystal structure of cot kinase domain in complex with 5-(2-amino-5-2 (quinolin-3-yl)pyridin-3-yl)-1,3,4-oxadiazole-2(3h)-thione
114	<a href="#">c2y7jB</a>	Alignment	not modelled	97.9	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphorylase b kinase gamma catalytic chain, testis/liver <b>PDBTitle:</b> structure of human phosphorylase kinase, gamma 2
115	<a href="#">c3e7eA</a>	Alignment	not modelled	97.9	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mitotic checkpoint serine/threonine-protein kinase bub1; <b>PDBTitle:</b> structure and substrate recruitment of the human spindle checkpoint2 kinase bub
116	<a href="#">c6fdzU</a>	Alignment	not modelled	97.9	13	<b>PDB header:</b> transferase <b>Chain:</b> U: <b>PDB Molecule:</b> serine/threonine-protein kinase ulk3; <b>PDBTitle:</b> unc-51-like kinase 3 (ulk3) in complex with momelotinib
117	<a href="#">c4bwxB</a>	Alignment	not modelled	97.9	13	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> pab-dependent poly(a)-specific ribonuclease subunit pan-3; <b>PDBTitle:</b> structure of neurospora crassa pan3 pseudokinase mutant
118	<a href="#">d1o6ya</a>	Alignment	not modelled	97.9	18	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
119	<a href="#">c2rsvA</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase vrk1; <b>PDBTitle:</b> solution structure of human full-length vaccinia related kinase 12 (vrk1)
120	<a href="#">c4fieB</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase pak 4; <b>PDBTitle:</b> full-length human pak4